

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bander, Neil H.

(ii) TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

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(F) ZIP: 14603-1051

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/016,976  
(B) FILING DATE: 06-MAY-1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 06/022,125  
(B) FILING DATE: 18-JUL-1996

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/838,632  
(B) FILING DATE: 09-APR-1997

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(C) REFERENCE/DOCKET NUMBER: 19603/1173

(xi) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTCCTGTCA GGAAC TGCAG GTG CTC TGAGG TCCAG CTG CAAC AGT CTGG ACCT GA	60
ACTGGTGAAG CCTGGGACTT CAGTGAGGAT ATCCTGCAAG ACTTCTGGAT ACACATT CAC	120
TGAATATAACC ATACACTGGG TGAAGCAGAG CCATGGAAAG AGCCTTGAGT GGATTGGAAA	180
CATCAATCCT AACAA TGGTG GTACCACCTA CAATCAGAAG TTCGAGGACA AGGCCACATT	240
GACTGTAGAC AAGTCCTCCA GTACAGCCTA CATGGAGCTC CGCAGCCTAA CATCTGAGGA	300
TTCTGCAGTC TATTATTGTG CAGCTGGTTG GAACTTGAC TACTGGGCC AAGGCACCAC	360
TCTCACAGTC TCCTCAGCCA AAACGACACC C	391

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTGTCGTT TTGGCTGAGG AGACTGTGAG AGTGGTGCCT TGGCCCCAGT AGTC AAGTT	60
CCAACCAAGCT GCACAATAAT AGACTGCAGA ATCCTCAGAT GTT AGGCTGC GGAGCTCCAT	120
GTAGGCTGTA CTGGAGGACT TGTCTACAGT CAATGTGGCC TTGTCCCGA ACTTCTGATT	180
GTAGGTGGTA CCACCATTGT TAGGATTGAT GTTCCAATC CACTCAAGGC TCTTCCATG	240
GCTCTGCTTC ACCCAGTGTA TGGTATATTG AGTGAATGTG TATCCAGAAG TCTTGCAGGA	300
TATCCTCACT GAAGTCCCAG GCTTCACCAG TTCAGGTCCA GACTGTTGCA GCTGGACCTC	360
AGAGAGGACA CCTGCAGTTC CTAGCAGGAG A	391

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Pro	Val	Arg	Asn	Cys	Arg	Cys	Pro	Leu	Gly	Pro	Ala	Ala	Thr	Val
1				5					10					15	
Trp	Thr	Thr	Gly	Glu	Ala	Trp	Asp	Phe	Ser	Glu	Asp	Ile	Leu	Gln	Asp
		20					25						30		
Phe	Trp	Ile	His	Ile	His	Ile	Tyr	His	Thr	Leu	Gly	Glu	Ala	Glu	Pro
		35				40						45			
Trp	Lys	Glu	Pro	Val	Asp	Trp	Lys	His	Gln	Ser	Gln	Trp	Trp	Tyr	His
	50				55					60					
Leu	Gln	Ser	Glu	Val	Arg	Gly	Gln	Gly	His	Ile	Asp	Cys	Arg	Gln	Val
	65				70				75				80		
Leu	Gln	Tyr	Ser	Leu	His	Gly	Ala	Pro	Gln	Pro	Asn	Ile	Gly	Phe	Cys
		85				90							95		
Ser	Leu	Leu	Leu	Cys	Ser	Trp	Leu	Glu	Leu	Leu	Leu	Gly	Pro	Arg	His
		100					105						110		
His	Ser	His	Ser	Leu	Leu	Ser	Gln	Asn	Asp	Thr					
		115					120								

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 130 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Leu	Ser	Gly	Thr	Ala	Gly	Val	Leu	Ser	Glu	Val	Gln	Leu	Gln	Gln
1				5				10				15			
Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Thr	Ser	Val	Arg	Ile	Ser	Cys
		20				25						30			
Lys	Thr	Ser	Gly	Tyr	Thr	Phe	Thr	Glu	Tyr	Thr	Ile	His	Trp	Val	Lys
		35				40						45			
Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly	Asn	Ile	Asn	Pro	Asn
		50				55					60				
Asn	Gly	Gly	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Glu	Asp	Lys	Ala	Thr	Leu
	65				70				75			80			
Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu
		85					90						95		
Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly	Trp	Asn	Phe
		100					105						110		

Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr  
115 120 125

Thr Pro  
130

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn  
1 5 10 15

Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg  
20 25 30

Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala  
35 40 45

Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val  
50 55 60

Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser  
65 70 75 80

Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu  
85 90 95

Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys  
100 105 110

Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro  
115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAGGTCCAGC TGCAACAGTC TGGACCTGAA CTGGTGAAGC CTGGGACTTC AGTGAGGATA 60  
TCCTGCAAGA CTTCTGGATA CACATTCACT GAATATACCA TACACTGGGT GAAGCAGAGC 120

CATGGAAAGA GCCTTGAGTG GATTGGAAAC ATCAATCCTA ACAATGGTGG TACCACCTAC	180
AATCAGAAGT TCGAGGACAA GGCCACATTG ACTGTAGACA AGTCCTCCAG TACAGCCTAC	240
ATGGAGCTCC GCAGCCTAAC ATCTGAGGAT TCTGCAGTCT ATTATTGTGC AGCTGGTTGG	300
AACTTTGACT ACTGGGGCCA AGGCACCACT CTCACAGTCT CCTCA	345

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAGGAGACT GTGAGAGTGG TGCCTTGGCC CCAGTAGTCA AAGTTCCAAC CAGCTGCACA	60
ATAATAGACT GCAGAATCCT CAGATGTTAG GCTGCGGAGC TCCATGTAGG CTGTACTGGA	120
GGACTTGTCT ACAGTCAATG TGGCCTTGTC CTCGAACCTTC TGATTGTAGG TGGTACCACC	180
ATTGTTAGGA TTGATGTTTC CAATCCACTC AAGGCTCTTT CCATGGCTCT GCTTCACCCA	240
GTTGTATGGTA TATTCAGTGA ATGTGTATCC AGAAAGTCTTG CAGGATATCC TCACTGAAGT	300
CCCAGGCTTC ACCAGTTCAAG GTCCAGACTG TTGCAGCTGG ACCTC	345

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr	
1 5 10 15	
Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr	
20 25 30	
Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile	
35 40 45	
Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe	
50 55 60	

Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80  
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr  
100 105 110  
Val Ser Ser  
115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTATATGGAG CTGATGGAA CATTGTAATG ACCCAATCTC CCAAATCCAT GTCCATGTCA 60  
GTAGGAGAGA GGGTCACCTT GACCTGCAAG GCCAGTGAGA ATGTGGTTAC TTATGTTCC 120  
TGGTATCAAC AGAAAACCAGA GCAGTCTCCT AACTGCTGA TATACTGGGC ATCCAACCGG 180  
TACACTGGGG TCCCCGATCG CTTCACAGGC AGTGGATCTG CAACAGATTT CACTCTGACC 240  
ATCAGCAGTG TGCAGGCTGA AGACCTTGCA GATTATCACT GTGGACAGGG TTACAGCTAT 300  
CCGTACACGT TCGGAGGGGG GACCAAGCTG GAAATAAAAC GGGCTGATGC TGCACCAA 360  
GTA 363

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACAGTTGGT GCAGCATCAG CCCGTTTAT TTCCAGCTTG GTCCCCCTC CGAACGTGTA 60  
CGGATAGCTG TAACCCCTGTC CACAGTGATA ATCTGCAAGG TCTTCAGCCT GCACACTGCT 120  
GATGGTCAGA GTGAAATCTG TTGCAGATCC ACTGCCTGTG AAGCGATCGG GGACCCCAGT 180

GTACCGGTTG GATGCCCGT ATATCAGCAG TTTAGGAGAC TGCTCTGGTT TCTGTTGATA	240
CCAGGAAACA TAAGTAACCA CATTCTCACT GGCCCTGCAG GTCAAGGTGA CCCTCTCTCC	300
TACTGACATG GACATGGATT TGGGAGATTG GGTCATTACA ATGTTCCCAT CAGCTCCATA	360
TAA	363

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser			
1	5	10	15
Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser			
20	25	30	
Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln			
35	40	45	
Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val			
50	55	60	
Pro Asp Arg Phe Thr Gly Ser Ala Thr Asp Phe Thr Leu Thr			
65	70	75	80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln			
85	90	95	
Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile			
100	105	110	
Lys Arg Ala Asp Ala Ala Pro Thr Val			
115	120		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 114 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro			
1	5	10	15

Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu  
20 25 30

Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys  
35 40 45

Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln  
50 55 60

Ala Val Asp Leu Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu  
65 70 75 80

Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr  
85 90 95

Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln  
100 105 110

Leu Tyr

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His  
1 5 10 15

Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu  
20 25 30

Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser  
35 40 45

Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser  
50 55 60

Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln  
65 70 75 80

Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu  
85 90 95

Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys  
100 105 110

Cys Thr Asn Cys  
115

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACATTGTAA TGACCCAATC TCCCAAATCC ATGTCCATGT CAGTAGGAGA GAGGGTCACC	60
TTGACCTGCA AGGCCAGTGA GAATGTGGTT ACTTATGTTT CCTGGTATCA ACAGAAACCA	120
GAGCAGTCTC CTAAACTGCT GATATAACGGG GCATCCAACC GGTACACTGG GGTCCCCGAT	180
CGCTTCACAG GCAGTGGATC TGCAACAGAT TTCACTCTGA CCATCAGCAG TGTGCAGGCT	240
GAAGACCTTG CAGATTATCA CTGTGGACAG GGTTACAGCT ATCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTATTTCC AGCTTGGTCC CCCCTCCGAA CGTGTACGGA TAGCTGTAAC CCTGTCCACA	60
GTGATAATCT GCAAGGTCTT CAGCCTGCAC ACTGCTGATG GTCAGAGTGA AATCTGTTGC	120
AGATCCACTG CCTGTGAAGC GATCGGGGAC CCCAGTGTAC CGGTTGGATG CCCC GTATAT	180
CAGCAGTTA GGAGACTGCT CTGGTTCTG TTGATACCAAG GAAACATAAG TAACCACATT	240
CTCACTGGCC TTGCAGGTCA AGGTGACCCCT CTCTCCTACT GACATGGACA TGGATTGAGG	300
AGATTGGGTC ATTACAATGT T	321

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Val Gly  
1 5 10 15

Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr  
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile  
35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly  
50 55 60

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala  
65 70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr  
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATTGTGA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC	60
ATCATCTGTA AGGCCAGTCA AGATGTGGGT ACTGCTGTAG ACTGGTATCA ACAGAAACCA	120
GGACAATCTC CTAAACTACT GATTTATTGG GCATCCACTC GGCACACTGG AGTCCCTGAT	180
CGCTTCACAG GCAGTGGATC TGGGACAGAC TTCACTCTCA CCATTACTAA TGTTCACTCT	240
GAAGACTTG G CAGATTATTT CTGTCAGCAA TATAACAGCT ATCCTCTCAC GTTCGGTGCT	300
GGGACCATGC TGGACCTGAA A	321

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTCAGGTCC AGCATGGTCC CAGCACCGAA CGTGAGAGGA TAGCTGTTAT ATTGCTGACA	60
GAAATAATCT GCCAAGTCTT CAGACTGAAC ATTAGTAATG GTGAGAGTGA AGTCTGTCCC	120
AGATCCACTG CCTGTGAAGC GATCAGGGAC TCCAGTGTGC CGAGTGGATG CCCAATAAAT	180
CAGTAGTTA GGAGATTGTC CTGGTTCTG TTGATACCAAG TCTACAGCAG TACCCACATC	240
TTGACTGGCC TTACAGATGA TGCTGACCCCT GTCTCCTACT GATGTGGACA TGAATTGTG	300
AGACTGGTC ATCACAAATGT C	321

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly			
1	5	10	15
Asp Arg Val Ser Ile Ile Cys Lys Ala Ser Gln Asp Val Gly Thr Ala			
20	25	30	
Val Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile			
35	40	45	
Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly			
50	55	60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Val Gln Ser			
65	70	75	80
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser Tyr Pro Leu			
85	90	95	
Thr Phe Gly Ala Gly Thr Met Leu Asp Leu Lys			
100	105		